

AMENDMENTS TO THE CLAIMS

1-9. (Canceled)

10. (Original) A method for identifying a subpopulation of polymers having a property in common with a sample polymer of chemical units, comprising:

- (A) applying an experimental constraint to the polymer to modify the polymer,
- (B) detecting a property of the modified polymer;
- (C) identifying a population of polymers of chemical units having the same molecular length as the sample polymer; and
- (D) identifying a subpopulation of the identified population of polymers having the same property as the modified polymer by eliminating, from the identified population of polymers, polymers having properties that do not correspond to the modified polymer.

11. (Original) The method of claim 10, further comprising repeating steps (A), (B), and (D) on the modified polymer to identify a second subpopulation within the subpopulation of polymers having a second property in common with the twice modified polymer.

12. (Original) The method of claim 11, further comprising repeatedly performing the steps (A), (B), and (D) on the modified polymer until the number of polymers within the subpopulation falls below a predetermined threshold.

13. (Original) The method of claim 12, wherein the predetermined threshold of polymers within the subpopulation is two polymers and wherein the method is performed to identify the sequence of the polymer.

14. (Original) The method of claim 12, wherein the experimental constraints applied to the polymer are different for each repetition.

15. (Original) The method of claim 10, wherein the experimental constraint applied to the polymer is digestion with an exoenzyme.
16. (Original) The method of claim 10, wherein the experimental constraint applied to the polymer is digestion with an endoenzyme.
17. (Original) The method of claim 10, wherein the experimental constraint applied to the polymer is selected from the group consisting of restriction endonuclease digestion; chemical digestion; chemical modification; interaction with a binding compound; chemical peeling; and enzymatic modification.
18. (Original) The method of claim 10, wherein the property of the polymer is molecular weight.
19. (Original) The method of claim 10, wherein the population of polymers of chemical units includes every polymer sequence having the molecular weight of the sample polymer.
20. (Original) The method of claim 10, wherein the population of polymers of chemical units includes less than every polymer sequence having the molecular weight of the sample polymer.
21. (Original) The method of claim 10, wherein the step of detection involves the use of mass spectrometry to determine the molecular weight of the polymer.
22. (Original) The method of claim 21, wherein the mass spectrometry is matrix assisted laser desorption ionization which detects molecular weight with an accuracy of approximately one Dalton.

23. (Original) The method of claim 10, wherein polymer is reduced to at least two fragments and the property of the polymer is the size of the fragments and wherein the step of detection involves strong ion exchange chromatography.

24. (Original) The method of claim 10, wherein the step of identifying includes selecting the population of polymers of chemical units from a database including molecular weights of polymers of chemical units.

25. (Original) The method of claim 24, wherein the database includes identifiers corresponding to chemical units of a plurality of polymers, each of the identifiers including a field storing a value corresponding to a property of the corresponding chemical unit.

26-31. (Canceled)

32. (Original) A method for sequencing a polymer, comprising:

- (A) applying an experimental constraint to the polymer to modify the polymer,
- (B) detecting a property of the modified polymer;
- (C) identifying a population of polymers having the same molecular length as the sample polymer and having molecular weights similar to the molecular weight of the sample polymer;
- (D) identifying a subpopulation of the identified population of polymers having the same property as the modified polymer by eliminating, from the identified population of polymers, polymers having properties that do not correspond to the modified polymer;
- (E) repeating steps (A), (B), and (D) by applying additional experimental constraints to the polymer and identifying additional subpopulations of polymers until the number of polymers within the subpopulation is one and the sequence of the polymer may be identified.

33-38. (Canceled)

39. (New) The method of claim 32, wherein the polymer is a polysaccharide.

40. (New) The method of claim 39, wherein the polysaccharide is a heparin-like-glycosaminoglycan.

41. (New) A method for identifying a subpopulation of polysaccharides having a property in common with a sample polysaccharide, comprising:

- (A) applying an experimental constraint to the polysaccharide to modify the polysaccharide,
- (B) detecting a property of the modified polysaccharide;
- (C) identifying a population of polysaccharides having the same molecular length as the sample polysaccharide; and
- (D) identifying a subpopulation of the identified population of polysaccharides having the same property as the modified polysaccharide by eliminating, from the identified population of polysaccharides, polysaccharides having properties that do not correspond to the modified polysaccharide.

42. (New) The method of claim 41, wherein the polysaccharide is a heparin-like-glycosaminoglycan.